

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:37:26 ; Search time 156 Seconds  
(without alignments)  
726.657 Million cell updates/sec

Title: US-09-403-882A-2

Perfect score: 1622

Sequence: 1 MAEYKLOESGGGLVQPGSR.....VVLTIISLILIMLWQKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1596664

Minimum DB seq length: 0

Maximum DB seq length: 316

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1622	100.0	316	2	AAY32086
2	1319	81.3	255	3	AAB11398
3	1319	81.3	255	4	AAB74199
4	1319	81.3	255	4	AAB70769
5	1319	81.3	255	4	AAY72020
6	1237	76.3	241	6	ABR62010
7	1227	75.6	241	5	AAM48925
8	1194	73.6	236	2	AAR32842
9	1185	73.1	240	2	AAR68613
10	1097.5	67.7	223	2	AAR32841
11	976.5	60.2	237	7	AAE38657
12	970.5	59.8	268	3	AAY44973
13	967.5	59.6	268	3	AAY44972
14	964.5	59.5	284	2	AAR95569
15	959	59.1	291	8	ADN06993
16	954	58.8	280	6	ABR42055
17	939	57.9	234	2	AAR64819
18	938.5	57.9	235	2	AAR32840
19	937.5	57.8	272	8	ADO19054
20	937	57.8	258	2	AAW90221
21	935.5	57.7	294	4	ABR20442
22	934.5	57.6	293	4	AAE65715
23	928.5	57.2	282	6	ABU19276
24	927	57.2	291	8	ADN06992
25	926	57.1	287	8	ADN06988

ALIGNMENTS

RESULT 1  
AAY32086  
ID AAY32086 standard; protein; 316 AA.  
XX  
AC AAY32086;  
XX  
DT 17-JAN-2000 (first entry)  
XX  
DE Single chain antibody used in probe detection.  
XX  
KW Single chain antibody; scAb; sFv; spectroscopic probe.  
XX  
OS Unidentified.  
XX  
PN WO9951986-A1.  
XX  
PD 14-OCT-1999.  
XX  
PF 08-APR-1999; 99WO-US007847.  
XX  
PR 08-APR-1998; 98US-0081118P.  
PR 09-APR-1998; 98US-0081340P.  
XX  
(REGC ) UNIV CALIFORNIA.  
FA  
Farinas J;  
XX  
WPI; 1999-611066/52.  
DR  
N-PSDB; AA220266.  
XX  
Localizing probes to specific sites in cells that express single-chain antibody reactive with probe-ligand conjugate, particularly for detecting post-translational modification and its modulators.  
XX  
Claim 5; Page 47-48; 69pp; English.  
XX  
The present sequence represents a single chain antibody (scAb) that has 2 c-myc epitopes. The scAb is used in claimed methods for localizing a probe and for detecting a post-translational activity in a cell, and is expressed by a claimed transgenic non-human animal. The invention provides methods and reagents for targeting probes to selected cellular locations through the expression of specific binding partners (such as scAbs) within a cell, and for creating assays for post-translational activities. The invention allows the monitoring of the location of such intracellular, specific binding patterns over time and in response to stimuli, such as test chemicals. Spectroscopic probes can be used to screen a test chemical for activity. The invention also includes cells and transgenic organisms comprising the intracellular specific binding

Adq75290 Immunoglo  
Abf62132 Single ch  
Adq75289 Immunoglo  
Abp46093 Human Bly  
Adg96920 Single ch  
Aaw90225 Anti-B7.1  
Abp46009 Human Bly  
Adg96836 Single ch  
Abp46103 Human Bly  
Abp45994 Human Bly  
Adg96930 Single ch  
Adg96821 Single ch  
Aaw82744 Fusion pr  
Adh50847 SGV RFB4  
Abp46107 Human Bly  
Adg96934 Single ch  
Abp46104 Human Bly  
Adg96931 Single ch  
Abp46100 Human Bly  
Abp46016 Human Bly

CC partner, where the specific binding partner can bind with the  
 CC spectroscopic probe/ligand conjugate. scAbs can be expressed within the  
 CC cell and can be designed to bind a wide variety of spectroscopic probes,  
 CC including small molecules that have better (and more diverse)  
 CC spectroscopic properties than green fluorescent protein  
 XX  
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1622; DB 2; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-108;  
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEVKLESGGGLVQPGSGRKLSCAASGFTFSSFGMHVVRQAPKGLWVAYISSGSTI 60  
 DB 1 MAEVKLESGGGLVQPGSGRKLSCAASGFTFSSFGMHVVRQAPKGLWVAYISSGSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYGAYWGQTTVTSSGGGG 120  
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYGAYWGQTTVTSSGGGG 120  
 QY 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 DB 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPPARFSGSGGTSTSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKEAA 240  
 DB 181 TSKLSSGVPPARFSGSGGTSTSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKEAA 240  
 QY 241 AEQKLISEEDLNGVDEQKLISEEDLNAVGDQTEVIVPHSLPKVVIISAIALVLT 300  
 DB 241 AEQKLISEEDLNGVDEQKLISEEDLNAVGDQTEVIVPHSLPKVVIISAIALVLT 300  
 QY 301 IISLIILIMLQKKPR 316  
 DB 301 IISLIILIMLQKKPR 316

## RESULT 2

AAB11398  
 ID AAB11398 standard; protein; 255 AA.  
 AC AAB11398;  
 DT 22-FEB-2001 (first entry)  
 DE E. coli expression plasmid PUBS520-ScFvOx encoded protein.  
 KW Eukaryotic protein; protease; interferon; antibody; hormone;  
 KW disulfide bridge.  
 OS Escherichia coli.  
 OS Synthetic.  
 XX  
 PN EP1048732-A1.  
 PD 02-NOV-2000.  
 PF 26-APR-1999; 99EP-00107412.  
 PR 26-APR-1999; 99EP-00107412.  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA WPI; 2000-674185/66.  
 DR N-PSDB; AAC66074.  
 XX  
 PT Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.  
 PS Example 6; Page 22-23; 40pp; German.  
 XX  
 CC This invention describes a novel preparation of a water-soluble,

CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain FV fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 CC naturation

SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 3; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-86;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAEVKLESGGGLVQPGSGRKLSCAASGFTFSSFGMHVVRQAPKGLWVAYISSGSTI 60  
 DB 1 MAEVKLESGGGLVQPGSGRKLSCAASGFTFSSFGMHVVRQAPKGLWVAYISSGSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYGAYWGQTTVTSSGGGG 120  
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYGAYWGQTTVTSSGGGG 120  
 QY 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 DB 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPPARFSGSGGTSTSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKEAA 240  
 DB 181 TSKLSSGVPPARFSGSGGTSTSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKEAA 240  
 QY 241 AEQKLISEEDLNGA 254  
 DB 241 AEQKLISEEDLNGA 254

## RESULT 3

AAB74199  
 ID AAB74199 standard; protein; 255 AA.  
 AC AAB74199;  
 DT 29-MAY-2001 (first entry)  
 DE PelB-scFvOxazolone fusion protein.  
 KW Molecular chaperone; PelB signal sequence; scFvOxazolone.  
 OS Unidentified.  
 XX  
 PN EP1077262-A1.  
 PD 21-FEB-2001.  
 PF 24-JUL-2000; 2000EP-00115839.  
 PR 29-JUL-1999; 99EP-00114811.  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 PI WPI; 2001-246712/26.  
 DR N-PSDB; AAF77806.  
 XX  
 PT Producing naturally folded eukaryotic proteins e.g. antibodies,  
 PT interferon, hormones or proteases that contain two or several cysteines  
 PT linked by disulfide bridges comprises co-expression of a molecular  
 PT chaperone.  
 XX

PS Disclosure; Page 19; 35pp; English.

XX The present invention relates to a method for production of a naturally

CC folded eukaryotic protein containing two or more cysteines linked by

CC disulfide bridges. The method comprises co-expression and secretion into

CC the periplasm of a molecular chaperone via an expression vector coding

CC for the chaperone. The expression vector also encodes a signal sequence.

CC The method is useful for producing a naturally folded eukaryotic protein

CC such as an antibody, antibody fragment, interferon, protein hormone or a

CC protease containing two or several cysteines linked by disulfide bridges.

CC The present sequence is a fusion protein composed of the PelB signal

CC sequence and ScFvOxazolon. This sequence was used in the method of the

CC present invention

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;

Best Local Similarity 99.2%; Pred. No. 1.1e-86;

Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLOESGGGLVOPGSGSRKLSCAASGFTTSSFGMHVWROAPEKGLEWVAYISSGSSTI 60

DB 1 MAEVKLOESGGGLVOPGSGSRKLSCAASGFTTSSFGMHVWROAPEKGLEWVAYISSGSSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCARYGAYWGQTTVTVSSGGGG 120

DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCARYGAYWGQTTVTVSSGGGG 120

QY 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCTCSASSSVRYMNFQOKSGTSPKRWIYD 180

DB 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCTCSASSSVRYMNFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPAFPFGSGSGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA 240

DB 181 TSKLSSGVPAFPFGSGSGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA 240

QY 241 AEQKLISEEDLNGA 254

DB 241 AEQKLISEEDLNGA 254

RESULT 4

AAB70769

ID AAB70769 standard; protein; 255 AA.

AC AAB70769;

XX 18-MAY-2001 (first entry)

XX Expression plasmid pUB8520-ScFvOx protein.

XX Chaperone protein; periplasm; antibody production; protein production;

XX interferon production; protease production.

XX Escherichia coli.

OS Synthetic.

XX EP1077263-A1.

PN 21-FEB-2001.

XX 29-JUL-1999; 99EP-00114811.

XX 29-JUL-1999; 99EP-00114811.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX WPI; 2001-204356/21.

DR N-PSDB; AAF61193.

XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by

PT simultaneous expression of a chaperone protein, allows simple recovery

PT from periplasm or medium.

XX Disclosure; Page 20-21; 36pp; German.

XX This invention describes a novel method for preparing a naturally folded

CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged

CC Cys residues by culturing prokaryotic cells that contain an expression

CC vector for (I) including a prokaryotic signal sequence at its N-terminus

CC and a nucleic acid (II) that secretes a chaperone protein (III) into the

CC periplasm. (I) is secreted into the periplasm or medium; the signal

CC peptide is then cleaved and (I) isolated from the periplasm or medium.

CC The method is used for production of antibody, interferon, protein

CC hormone or protease. Expression of (III) increases the yield of (I). The

CC method is simple and eliminates time-consuming in vitro processing

CC operations such as dissolution of inclusion bodies, reduction and

CC refolding. (III) protects (I) against agglomeration and promotes their

CC natural conformation

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;

Best Local Similarity 99.2%; Pred. No. 1.1e-86;

Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLOESGGGLVOPGSGSRKLSCAASGFTTSSFGMHVWROAPEKGLEWVAYISSGSSTI 60

DB 1 MAEVKLOESGGGLVOPGSGSRKLSCAASGFTTSSFGMHVWROAPEKGLEWVAYISSGSSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCARYGAYWGQTTVTVSSGGGG 120

DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCARYGAYWGQTTVTVSSGGGG 120

QY 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCTCSASSSVRYMNFQOKSGTSPKRWIYD 180

DB 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCTCSASSSVRYMNFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPAFPFGSGSGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA 240

DB 181 TSKLSSGVPAFPFGSGSGTSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA 240

QY 241 AEQKLISEEDLNGA 254

DB 241 AEQKLISEEDLNGA 254

RESULT 5

AAY72020

ID AAY72020 standard; protein; 255 AA.

XX AC AAY72020;

XX 28-MAR-2001 (first entry)

XX E. carotovora PelB-scFvOx fusion protein encoded by PUBS520-pIN-scFvOx.

XX Secreted protein; chaperone; interferon; protease; hormone;

XX naturally folded protein; lac promoter; DnaJ; heat shock protein; HSP;

XX pectate lyase B; PelB; haptin; single-chain Fv-fragment Oxazolon;

XX scFvOxazolon; fusion protein; thyroid stimulating hormone; TSH.

XX Pectobacterium carotovorum.

OS Unidentified.

OS Chimeric.

XX EP1054063-A2.

XX 22-NOV-2000.

XX 19-APR-2000; 2000EP-00108505.

XX 26-APR-1999; 99EP-00107412.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 XX WPI; 2001-033777/05.  
 DR N-PSDB; AAD02212.  
 XX  
 PT Producing water-soluble, naturally folded, and secreted eukaryotic  
 PT polypeptide, involves culturing prokaryotic cells containing an  
 PT expression vector encoding the polypeptide in the presence of arginine or  
 PT a specific compound.  
 XX  
 PS Example 6; Page 22-23; 35pp; English.  
 XX  
 CC The patent discloses a method for the production of a water-soluble,  
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.  
 CC The method involves culturing the prokaryotic cells, containing an  
 CC expression vector encoding the desired protein and the prokaryotic signal  
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal  
 CC sequence mediates the secretion of the desired protein into the  
 CC periplasm, where folding of the protein takes place. The prokaryotic cell  
 CC also contains an expression vector encoding a molecular chaperone, e.g.,  
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-  
 CC overexpression and co-secretion of molecular chaperones in the periplasm  
 CC improves the yield of functionally folded protein. The above method  
 CC recombinantly produces a high yield of eukaryotic secreted proteins in  
 CC prokaryotes. The method is useful for producing eukaryotic proteins such  
 CC as an antibody, antibody fragment, interferon, protein hormone or a  
 CC protease. The present sequence is an Erwinia carotovora pectate lyase B  
 CC (PelB) signal sequence-scFvOx fusion protein encoded by PUBS520-PIN-  
 CC scFvOx. The plasmid, PUBS520-PIN-scFvOx, also comprises the lac promoter.  
 CC The single-chain Fv-fragment, which is directed against the haptan  
 CC oxazolon (ScfvOxazolon), is an antibody fragment against thyroid  
 CC stimulating hormone (TSH). The co-expression of ScFvOx which has no  
 CC chaperone properties is used as a negative control  
 XX  
 SQ Sequence 255 AA;  
 Query Match 81.3%; Score 1319; DB 4; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-86;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAEVLQESGGGLVPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSSTI 60  
 Db 1 MAEVLQESGGGLVPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSSTI 60  
 QY 61 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGGTTVTVSSGGGG 120  
 Db 61 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGGTTVTVSSGGGG 120  
 QY 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQOKSGTSPKRWIYD 180  
 Db 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQOKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPAFPFSGSGSTSYSLTSSMEAEADAATYYCQOWSSNPLTFGAGTKLELKRAA 240  
 Db 181 TSKLSSGVPAFPFSGSGSTSYSLTSSMEAEADAATYYCQOWSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEQKLISEEDLNGA 254  
 Db 241 AEQKLISEEDLNGA 254  
 RESULT 6  
 ABR62010  
 ID ABR62010 standard; protein; 241 AA.  
 XX  
 AC ABR62010;  
 XX  
 DT 03-OCT-2003 (first entry)  
 XX  
 DE Single-chain (scFv) antibody.  
 XX  
 KW Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy;  
 KW antisense therapy; scFv; antibody.

XX Synthetic.  
 OS  
 XX EPI321524-A1.  
 PN  
 XX 25-JUN-2003.  
 PD  
 XX 19-DEC-2001; 2001EP-00130319.  
 PF  
 XX 19-DEC-2001; 2001EP-00130319.  
 PR  
 XX (DUER/) DUERING K.  
 PA  
 XX Mahn A, Hantke S, Petsch D;  
 PI  
 XX WPI; 2003-543829/52.  
 DR  
 XX N-PSDB; ACC84876.  
 DR  
 XX  
 PT Increasing the content of transgene-coded biomolecules in a plant or  
 PT animal, useful for producing proteins for diagnosing, preventing and/or  
 PT treating viral diseases and cancer, comprises changing the distribution  
 PT of ATP and/or ADP.  
 XX  
 PS Example 2; Fig 2; 18pp; English.  
 PS  
 XX The invention relates to increasing the content of one or more transgene-  
 CC coded biomolecules in an organism and involves changing the distribution  
 CC of ATP and/or ADP in cells of the organism. The yield of transgenic  
 CC molecules in host cells is often insufficient for industrial production.  
 CC The method increases the yield of transgenic molecules in animal and  
 CC plant host cells, therefore facilitating their production on an  
 CC industrial scale. The proteins produced by the method are useful for  
 CC diagnosing, preventing and/or treating viral diseases and cancer. The  
 CC present sequence represents a single-chain (scFv) antibody, used to  
 CC exemplify the increase in the expression of scFv antibodies in transgenic  
 CC potato tubers  
 XX  
 SQ Sequence 241 AA;  
 Query Match 76.3%; Score 1237; DB 6; Length 241;  
 Best Local Similarity 97.9%; Pred. No. 8.1e-81;  
 Matches 235; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AEVLQESGGGLVPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSSTIY 61  
 Db 2 ADVQLVESGGGLVPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSSTIY 61  
 QY 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGGTTVTVSSGGGG 121  
 Db 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGGTTVTVSSGGGG 121  
 QY 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQOKSGTSPKRWIYD 181  
 Db 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQOKSGTSPKRWIYD 181  
 QY 182 SKLSSGVPAFPFSGSGSTSYSLTSSMEAEADAATYYCQOWSSNPLTFGAGTKLELKRAA 241  
 Db 182 SKLSSGVPAFPFSGSGSTSYSLTSSMEAEADAATYYCQOWSSNPLTFGAGTKLELKRAA 241  
 RESULT 7  
 AAM48925  
 ID AAM48925 standard; protein; 241 AA.  
 XX  
 AC AAM48925;  
 XX  
 DT 03-MAY-2002 (first entry)  
 XX  
 DE scFv antibody.  
 XX  
 KW Ketone binding protein; oxazole; pathogen resistance; virucide;  
 KW fungicide; antibacterial; scFv antibody.



Db 181 KLSSGVPARFSGSGTYSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELK 235

RESULT 9  
AAR68613  
ID AAR68613 standard; protein; 240 AA.  
XX  
AC AAR68613;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-SEP-1995 (first entry)  
XX  
DE Single chain antibody (scFv) which binds to phenylloxazolone.  
XX  
KW Genetic selection; ligand binding protein; cholera toxin; promoter;  
KW detection; selection; beta galactosidase; lac; transmembrane domain;  
KW regulatory domain; ds.  
XX  
OS Synthetic.  
XX  
XX DE4319296-A1.  
XX  
PD 15-DEC-1994.  
XX  
XX 10-JUN-1993; 93DE-04319296.  
XX  
XX 10-JUN-1993; 93DE-04319296.  
XX  
PA (BEHW ) BEHRINGWERKE AG.  
XX  
XX Fritz H, Hennecke F, Kolmar H;  
XX  
XX WPI; 1995-023689/04.  
DR N-PSDB; AAQ80468.  
XX  
XX Genetic selection of ligand binding proteins in microorganisms - by  
PT extracytoplasmic protein presentation, then use of ligand binding to  
PT express a detectable or selectable function.  
XX  
PS Example 2.2; Fig 4; 25pp; German.  
XX  
CC Genetic selection in microorganisms, for ligand binding proteins (LBP)  
CC comprises: extracytoplasmic presentation of LBP and; using the signal of  
CC ligand binding (by signal transduction on the biosynthetic machinery of  
CC the microorganisms) to express a detectable or selectable function.  
CC Microorganisms for this process include a genetically stable  
CC detection/selection and are transformed with a replicon encoding a fusion  
CC protein consisting of the LBP, a transmembrane helix and regulatory  
CC domain. The detection/selection function is expression of a beta-  
CC galactosidase gene, integrated into the chromosome and under the control  
CC of the ctx (cholera toxin) promoter. The transmembrane helix is taken  
CC from the toxR gene. Four primers (AAQ80457-60) were used in the  
CC construction of the plasmid pKTOXSCFV. The primers described in AAQ80457  
CC chain antibody NQ10.12.5 and those described in AAQ80459-60 were used to  
CC amplify the corresponding light chain sequence from the same antibody.  
CC The amplified sequences were cloned into the plasmid pKTOXREI (see  
CC AAQ80454-56 for details) to create a toxR-scFv fusion gene. This sequence  
CC is the single chain antibody (scFv). (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
XX Sequence 240 AA;  
SQ

Query Match  
Best Local Similarity 73.1%; Score 1185; DB 2; Length 240;  
Matches 225; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 4 VKLQESGGGLVQPGGSRKLSCAASGTFSSFGHWHVRQAPKGLWVAYISSGSTIYYA 63  
Db 6 VQLVELGGGVQPGGSRKLSCAASGTFSSFGHWHVRQAPKGLWVAYISSGSTIYYA 65  
QY 64 DTVKGRFTISRDNPKNTLFLQMTLSRSEDATMYCARYDYGAYWGQGLTVTVSSGGSGG 123

Db 66 DTVKGRFTISRDNPKNTLFLQMTLSRSEDATMYCARYDYGAYWGQGLTVTVSSGGSGG 125

QY 124 GSGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYNNWFQKSGTSPKRWIYDTSK 183  
|||||  
Db 126 GSGGGGSIQVLTQSPAIMSASGERVTMTCSASSSVRYNNWFQKSGTSPKRWIYDTSK 185  
|||||

QY 184 LSSGVPARFSGSGTYSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELK 238  
|||||  
Db 186 LSSGVPARFSGSGTYSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLELK 240

RESULT 10  
AAR32841  
ID AAR32841 standard; protein; 223 AA.  
XX  
AC AAR32841;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-JUN-1993 (first entry)  
XX  
DE VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences.  
XX  
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;  
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;  
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;  
KW NQ2/12.4; NQ10/12.5.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Region 1..114  
FT Peptide /label= VH\_NQ10/12.5  
FT Peptide 115..116  
FT Region /note= "Linker peptide"  
FT Region 117..223  
FT /label= Vkappa\_NQ10/12.5  
PN WO9303151-A1.  
XX  
PD 18-FEB-1993.  
XX  
XX 10-AUG-1992; 92WO-GB001483.  
XX  
PR 10-AUG-1991; 91GB-00017352.  
PR 11-JUN-1992; 92GB-00012419.  
XX  
XX (MEDI-) MEDICAL RES COUNCIL.  
XX  
PI Embleton MJ, Gorochov G, Jones PT, Winter GP;  
XX WPI; 1993-076508/09.  
DR N-PSDB; AAQ37460.  
XX  
PT Treatment of cell populations, partic. hybridomas - to link together  
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.  
XX  
PS Disclosure; Fig 3; 72pp; English.  
XX  
CC The sequences given in AAR32840-43 show the mature heavy chain VH domains  
CC and the Vk light chain genes of the antiphenyloxazolone hybridomas  
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-  
CC cell PCR. The cDNA encoding these peptides was synthesised using forward  
CC primers annealing to the Ck gene and the JH segment, followed by assembly  
CC with linker primers, VH back primers based on the VH3 leader sequence and  
CC a forward Ck primer, nested in respect to the primer used for cDNA. The  
CC assembled product within the cells is then amplified with nested primers  
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.  
CC In-cell PCR may be used to determine gene linkage analysis, particularly  
CC for the cloning of gene combinations that are polymorphic within a  
CC population of cells, such as the rearranged genes for Ig or TCR V  
CC regions. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 223 AA;  
SQ

```
Query Match      67.7%; Score 1097.5; DB 2; Length 223;
Best Local Similarity 90.2%; Pred. No. 7.6e-71;
Matches 212; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

QY 3 EVKLQESGGGLVOPGSGRKLSCAASGFTFSFGMHVWVQAPEKGLEWYVAYISSGSSSTIYY 62
DB 1 DVQLVESGGGLVOPGSGRKLSCAASGFTFSFGMHVWVQAPEKGLEWYVAYISSGSSSTIYY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWQGGTIVTVSSGGSGG 122
DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAYWQGGTIVTVSSA----- 114
QY 123 GGGSGGGSDIELTQSPAIMASPGERVMTCTCASSSVRYMNVFQKSGTSPKRWIYDTS 182
DB 115 -----ASQIVLTQSPAIMASPGERVMTCTCASSSVRYMNVFQKSGTSPKRWIYDTS 167
QY 193 KLSSGVPARFSGSGSGTSLTISMEAEADAATYYCQOWSSNPLTFGAGTKLELK 237
DB 168 KLSSGVPARFSGSGSGTSLTISMEAEADAATYYCQOWSSNPLTFGAGTKLELK 222

RESULT 11
AAE38657
ID AAE38657 standard; protein; 237 AA.
AC AAE38657;
DT 04-DEC-2003 (first entry)
XX
XX Mouse G1 single chain Fv-recombinant antibody.
DE
XX Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;
KW viral infection; autoimmune disease; gene therapy; cytostatic; virucide;
KW immunomodulator; mouse.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 1..118
FT Domain /note= "VH domain"
FT Region 31..35
FT /note= "Complementarity determining region"
FT Region 50..66
FT /note= "Complementarity determining region"
FT Region 99..108
FT /note= "Complementarity determining region"
FT Region 119..234
FT /note= "Peptide linker"
FT Domain 135..237
FT /note= "VL domain"
FT Region 158..167
FT /note= "Complementarity determining region"
FT Region 182..189
FT /note= "Complementarity determining region"
FT Region 222..230
FT /note= "Complementarity determining region"
FT
FT
XX WO2003068201-A2.
XX
XX 21-AUG-2003.
XX
XX 11-FEB-2003; 2003WO-IL000105.
XX
XX 13-FEB-2002; 2002US-00073301.
XX
XX (TECR ) TECHNION RES & DEV FOUND LTD.
XX
XX Reiter Y, Denkberg G;
XX
XX WPI; 2003-689603/65.
XX
XX N-PSDB; AAD58607.
XX
XX
```

```
PT New isolated molecule comprising an antibody that binds with a human
PT major histocompatibility complex (MHC) class I being complexed with a HLA
PT -restricted antigen, useful for treating cancer, viral infection or
PT autoimmune disease.
XX
XX Claim 63; Fig 3a; 81pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX specifically bindable with a binding affinity below 20 nanomolar to a
XX human major histocompatibility complex (MHC) class I being complexed with
XX a HLA-restricted antigen. The molecules, antibodies, and methods are
XX useful for treating cancer, viral infection and an autoimmune disease.
XX The invention is useful in gene therapy. The present sequence is mouse G1
XX single chain Fv-recombinant antibody
XX
XX Sequence 237 AA;

Query Match      60.2%; Score 976.5; DB 7; Length 237;
Best Local Similarity 78.9%; Pred. No. 3.9e-62;
Matches 187; Conservative 18; Mismatches 27; Indels 5; Gaps 1;

QY 3 EVKLQESGGGLVOPGSGRKLSCAASGFTFSFGMHVWVQAPEKGLEWYVAYISSGSSSTIYY 62
DB 1 QVKLQESGGGLVOPGSGRKLSCAASGFTFSFGMHVWVQAPEKGLEWYVAYISSGSSSTIYY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARD-----YGAYWQGGTIVTVSSG 117
DB 61 PDSVKGRFTISRDNPKNTLYLQMSLSKSEDVWYICARGNWEWYFDVWQGGTIVTVSSG 120
QY 118 GGGSGGGSGGGSDIELTQSPAIMASPGERVMTCTCASSSVRYMNVFQKSGTSPKRW 177
DB 121 GGGSGGGSGGGSDIELTQSPAIMASPGERVMTCTCASSSVRYMNVFQKSGTSPKRW 180
QY 178 IYDTSKLSSGVPARFSGSGSGTSLTISMEAEADAATYYCQOWSSNPLTFGAGTKL 234
DB 181 IYDTSNVAQVPRFPRFSGSGSGTSLTINMEAEADAATYYCQWESGYPTFGGGTKL 237

RESULT 12
AAE44973
ID AAY44973 standard; protein; 268 AA.
XX
XX AAY44973;
AC AAY44973;
DT 23-MAY-2000 (first entry)
XX
XX Recombinant mouse anti-rotavirus antibody (Clone 22) .
DE
XX
XX Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;
KW VH; light chain variable region; VL; pCANTAB 5E vector; treatment;
KW probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;
KW immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
XX
XX Synthetic.
OS Mus sp.
XX
XX Key Location/Qualifiers
FH 6..116
FT Region /label= Mouse_Heavy_chain_variable_region
FT Region 117..152
FT /label= Linker_region
FT Region 153..250
FT /label= Mouse_Light_chain_variable_region
FT Domain 254..266
FT /label= E_tag_domain
FT /note= "Enables immunodetection and immunoaffinity
FT purification of the recombinant antibody"
XX
XX WO200006764-A1.
XX
XX 10-FEB-2000.
XX
XX 29-JUL-1999; 99WO-US017296.
XX
XX
```

```

XX 30-JUL-1998; 98US-0094697P.
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;
XX
XX WPI; 2000-195315/17.
XX N-PSDB; AA250509.
XX
XX Composition for supplementing or replacing an immune response against
XX gastrointestinal pathogens in e.g. newborn infants, comprises probiotic
XX microorganisms expressing antibodies specific for the gastrointestinal
XX pathogens.
XX
XX Disclosure; Fig 2; 48pp; English.
XX
XX The present sequence is the recombinant mouse anti-rotavirus antibody. It
XX comprises of mouse heavy chain (VH) and light chain (VL) variable regions
XX joined by a linker. The recombinant antibody encoding DNA is inserted
XX into pCANTAB 5E expression vector (clone 22). The vector is used to
XX transform probiotic bacteria like, Lactobacilli for expression and
XX secretion of recombinant anti-rotavirus antibodies. The antibodies have
XX antibacterial and antiviral activity. Antibody-expressing probiotic
XX bacteria can be administered for treatment of gastrointestinal (GI) tract
XX infections and to immunise neonates, humans or immunosuppressed/
XX immunodeficient adults acutely exposed to a bolus of GI pathogen
XX
XX Sequence 268 AA;
XX
XX Query Match 59.8%; Score 970.5; DB 3; Length 268;
XX Best Local Similarity 74.7%; Pred. No. 1.2e-61;
XX Matches 186; Conservative 24; Mismatches 30; Indels 9; Gaps 3;
XX
XX QY 1 MAEVKLOESGGGLVPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTI 60
XX Db 6 MAQVQLQSGGGGLVPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTL 65
XX
XX QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYCARDYG-----AYWQGQTTVT 113
XX Db 66 HYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYCARDYG-----AYWQGQTTVT 124
XX
XX QY 114 VSSGGGGGGGGGGGGSDIELTQSPAIMSASFGERVMTWTCSSSV-RYMNWFOOKSGT 172
XX Db 125 VSSGGGGGGGGGGGGSDIVLTQSPASLSASVGETVITCRASENIYSYLAWYQKQKG 184
XX
XX QY 173 SPKRWIYDTSKLSGVPARFSGSGGTSYSLTISMEAEADAATYCCQWSNPLTFGAGT 232
XX Db 185 SPQFLVYSAKTLAGVPRFSGSGGTQFSLKINSLOPEDFGNYCYQHYYGSPRTFGAGT 244
XX
XX QY 233 KLELKRAAA 241
XX Db 245 KLELKRAAA 253
XX
XX RESULT 13
XX AA44972
XX ID AA44972 standard; protein; 268 AA.
XX AC
XX AY44972;
XX
XX 23-MAY-2000 (first entry)
XX
XX Recombinant mouse anti-rotavirus antibody (Clone 11).
XX
XX Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;
XX VH; light chain variable region; VL; pCANTAB 5E vector; treatment;
XX probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;
XX immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
XX
XX Synthetic.
XX Mus sp.

```

```

FH Key Location/Qualifiers
FT Region 6..116
FT /label= Mouse_Heavy_chain_variable_region
FT Region 117..151
FT /label= Linker_region
FT Region 152..250
FT /label= Mouse_Light_chain_variable_region
FT Domain 254..266
FT /label= E_tag_domain
FT /notes= "Enables immunodetection and immunoaffinity
FT purification of the recombinant antibody"
XX
XX WO200006764-A1.
XX
XX 10-FEB-2000.
XX
XX 29-JUL-1999; 99WO-US017296.
XX
XX 30-JUL-1998; 98US-0094697P.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;
XX
XX WPI; 2000-195315/17.
XX N-PSDB; AA250508.
XX
XX Composition for supplementing or replacing an immune response against
XX gastrointestinal pathogens in e.g. newborn infants, comprises probiotic
XX microorganisms expressing antibodies specific for the gastrointestinal
XX pathogens.
XX
XX Disclosure; Fig 1; 48pp; English.
XX
XX The present sequence is the recombinant mouse anti-rotavirus antibody. It
XX comprises of mouse heavy chain (VH) and light chain (VL) variable regions
XX joined by a linker. The recombinant antibody encoding DNA is inserted
XX into pCANTAB 5E expression vector (clone 11). The vector is used to
XX transform probiotic bacteria like, Lactobacilli for expression and
XX secretion of recombinant anti-rotavirus antibodies. The antibodies have
XX antibacterial and antiviral activity. Antibody-expressing probiotic
XX bacteria can be administered for treatment of gastrointestinal (GI) tract
XX infections and to immunise neonates, humans or immunosuppressed/
XX immunodeficient adults acutely exposed to a bolus of GI pathogen
XX
XX Sequence 268 AA;
XX
XX Query Match 59.6%; Score 967.5; DB 3; Length 268;
XX Best Local Similarity 75.1%; Pred. No. 2e-61;
XX Matches 187; Conservative 22; Mismatches 31; Indels 9; Gaps 3;
XX
XX QY 1 MAEVKLOESGGGLVPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTI 60
XX Db 6 MAQVQLQSGGGGLVPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTL 65
XX
XX QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYCARDYG-----AYWQGQTTVT 113
XX Db 66 HYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYCARDYG-----AYWQGQTTVT 124
XX
XX QY 114 VSSGGGGGGGGGGGGSDIELTQSPAIMSASFGERVMTWTCSSSV-RYMNWFOOKSGT 172
XX Db 125 VSSGGGGGGGGGGGGSDIVLTQSPASLSASVGETVITCRASENIYSYLAWYQKQKG 184
XX
XX QY 173 SPKRWIYDTSKLSGVPARFSGSGGTSYSLTISMEAEADAATYCCQWSNPLTFGAGT 232
XX Db 185 SPQFLVYSAKTLAGVPRFSGSGGTQFSLKINSLOPEDFGNYCYQHYYGSPRTFGAGT 244
XX
XX QY 233 KLELKRAAA 241
XX Db 245 KLELKRAAA 253
XX
XX RESULT 14

```





Db 141 VTVSSGGGGGGGGGGSEIVLTQSPSSLSASVGRVTITCRASQSISSYLNWYQQK 200  
QY 171 GTSPPRWIYDTSKLSGGVPAFPSSGGSGTYSYSLTISMEAEADAATYYCQOWSSNPLTFGA 230  
Db 201 GKAPKLLIYAASSLOSQGVFSRFSGGSGTFTLTISLQDDDFATYYCQYNSYPWTFGQ 260  
QY 231 GTKLELKRAAAEQKLISEEDLNGA 254  
Db 261 GTKLEIKRAAAEQKLISEEDLNGA 284

Search completed: December 30, 2004, 15:51:37  
Job time : 164 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:49:07 ; Search time 38 Seconds  
(without alignments)  
551.487 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVLQESGGGLVQPGGSR.....VLTFTISJILMLWQKXPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 410336

Minimum DB seq length: 0  
Maximum DB seq length: 316

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319	81.3	255	US-09-553-498-8	Sequence 8, Appli
2	1319	81.3	255	US-09-618-869-8	Sequence 8, Appli
3	1199	73.9	236	US-08-190-199A-65	Sequence 65, Appl
4	1185	73.1	240	US-08-956-047-25	Sequence 25, Appl
5	1102.5	68.0	223	US-08-190-199A-63	Sequence 63, Appl
6	964.5	59.5	284	US-08-564-164A-2	Sequence 2, Appli
7	943.5	58.2	235	US-08-190-199A-61	Sequence 61, Appl
8	900.5	55.5	281	US-09-423-439-44	Sequence 44, Appl
9	897.5	55.3	245	US-09-138-091A-76	Sequence 76, Appl
10	894	55.1	240	US-09-192-854-2	Sequence 2, Appli
11	890.5	54.9	245	US-08-918-148-75	Sequence 75, Appl
12	890.5	54.9	245	US-08-918-148-78	Sequence 78, Appl
13	890.5	54.9	245	US-09-138-091A-73	Sequence 73, Appl
14	881.5	54.3	245	US-08-918-148-76	Sequence 76, Appl
15	881.5	54.3	245	US-09-138-091A-74	Sequence 74, Appl
16	877	54.1	270	US-08-652-507-2	Sequence 2, Appli
17	873.5	53.9	301	US-08-661-052-14	Sequence 14, Appl
18	873.5	53.9	301	US-09-188-082-14	Sequence 14, Appl
19	873.5	53.9	301	US-09-364-088-14	Sequence 14, Appl
20	873.5	53.9	301	US-09-102-716-14	Sequence 14, Appl
21	864	53.3	258	US-09-526-738A-4	Sequence 4, Appli
22	861	53.1	239	US-08-279-772A-8	Sequence 8, Appli
23	861	53.1	239	US-08-902-486-11	Sequence 11, Appl
24	861	53.1	282	US-08-860-174A-10	Sequence 10, Appl
25	858.5	52.9	284	US-09-184-658-40	Sequence 40, Appl
26	858.5	52.9	284	US-09-504-262D-40	Sequence 40, Appl
27	855	52.7	244	US-08-918-148-77	Sequence 77, Appl

28	855	52.7	244	4	US-09-138-091A-75	Sequence 75, Appl
29	855	52.7	256	4	US-09-526-738A-2	Sequence 2, Appli
30	853.5	52.6	242	2	US-08-553-497A-26	Sequence 26, Appl
31	851	52.5	246	1	US-08-469-486-57	Sequence 57, Appl
32	851	52.5	246	2	US-08-469-658-57	Sequence 57, Appl
33	847	52.2	222	2	US-08-190-199A-67	Sequence 67, Appl
34	840.5	51.8	244	2	US-08-553-497A-20	Sequence 20, Appl
35	838.5	51.7	242	2	US-08-553-497A-28	Sequence 28, Appl
36	836.5	51.6	244	2	US-08-553-497A-22	Sequence 22, Appl
37	834	51.4	310	3	US-09-079-029-11	Sequence 11, Appl
38	829	51.1	289	3	US-09-184-658-63	Sequence 63, Appl
39	829	51.1	289	3	US-09-504-262D-63	Sequence 63, Appl
40	828	51.0	239	2	US-08-553-497A-18	Sequence 18, Appl
41	819.5	50.5	246	2	US-08-553-497A-24	Sequence 24, Appl
42	815.5	50.3	267	3	US-09-485-737B-2	Sequence 2, Appli
43	813.5	50.2	240	1	US-08-488-113B-148	Sequence 148, App
44	813.5	50.2	240	1	US-08-477-484B-148	Sequence 148, App
45	813.5	50.2	240	2	US-08-646-360-148	Sequence 148, App

ALIGNMENTS

RESULT 1  
US-09-553-498-8  
; Sequence 8, Application US/09553498  
; Patent No. 6309861  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorothee  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: Process for the production of naturally folded and secreted protein  
; FILE REFERENCE: Case 20379  
; CURRENT APPLICATION NUMBER: US/09/553,498  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: EP99107412.1  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 8  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: E. coli  
US-09-553-498-8

Query Match	81.3%	Score 1319;	DB 3;	Length 255;
Best Local Similarity	99.2%	Pred: No. 8e-91;	Mismatches 1;	Indels 0; Gaps 0;
Matches 252;	Conservative			
Qy	1	MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI	60	
Db	1	MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSTI	60	
Qy	61	YYADTVKGRFTISRDNPNTLFLQWTSLSRSDTVMYYCARDYGATWGQGTTVTVSSGGGG	120	
Db	61	YYADTVKGRFTISRDNPNTLFLQWTSLSRSDTVMYYCARDYGATWGQGTTVTVSSGGGG	120	
Qy	121	SGGGSGGGGDIETQSPATMSAPGERVTMTCSASSVRYMNVFQOKSGTSPKRWLYD	180	
Db	121	SGGGSGGGGDIETQSPATMSAPGERVTMTCSASSVRYMNVFQOKSGTSPKRWLYD	180	
Qy	181	TSKLSGVPARFSGSGGTSLYLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA	240	
Db	181	TSKLSGVPARFSGSGGTSLYLTSSMEADAATYYCQWSSNPLTFGAGTKLELKRAA	240	
Qy	241	AEQKLISEEDLNGA	254	
Db	241	AEQKLISEEDLNGA	254	

RESULT 2  
US-09-618-869-8  
; Sequence 8, Application US/09618869

```
/ Patent No. 6455279
/ GENERAL INFORMATION:
/ APPLICANT: Ambrosius, Dorthée
/ APPLICANT: Rudolph, Rainer
/ APPLICANT: Schaeffner, Joerg
/ APPLICANT: Schwarz, Elisabeth
/ TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
/ TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
/ TITLE OF INVENTION: CHAPERONES
/ FILE REFERENCE: 20381
/ CURRENT APPLICATION NUMBER: US/09/618,869
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: EP99114811.5
/ PRIOR FILING DATE: 1999-07-29
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 255
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-09-618-869-8

Query Match      81.3%; Score 1319; DB 4; Length 255;
Best Local Similarity 99.2%; Pred. No. 8e-91;
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEYKQESGGGLVQPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAISSGSTI 60
DB 1 MAEYKQESGGGLVQPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAISSGSTI 60
QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQTTVTYSSGGGG 120
DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQTTVTYSSGGGG 120
QY 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYD 180
DB 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYD 180
QY 181 TSKLSSGVPARFSGSGGTYSYLTSSMEAEADATYYCQWSSNPLTFGAGTKLEKRAA 240
DB 181 TSKLSSGVPARFSGSGGTYSYLTSSMEAEADATYYCQWSSNPLTFGAGTKLEKRAA 240
QY 241 AEQKLISEEDLNGA 254
DB 241 AEQKLISEEDLNGA 254

RESULT 3
US-08-190-199A-65
/ Sequence 65, Application US/08190199A
/ Patent No. 5830663
/ GENERAL INFORMATION:
/ APPLICANT: EMBLETON, Michael J.
/ APPLICANT: GOROCHOV, Guy
/ APPLICANT: JONES, Peter T.
/ APPLICANT: WINTER, Gregory P.
/ TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/190,199A
/ FILING DATE: 13-JUL-1994

/ Patent No. 6455279
/ GENERAL INFORMATION:
/ APPLICANT: Ambrosius, Dorthée
/ APPLICANT: Rudolph, Rainer
/ APPLICANT: Schaeffner, Joerg
/ APPLICANT: Schwarz, Elisabeth
/ TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
/ TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
/ TITLE OF INVENTION: CHAPERONES
/ FILE REFERENCE: 20381
/ CURRENT APPLICATION NUMBER: US/09/618,869
/ CURRENT FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: EP99114811.5
/ PRIOR FILING DATE: 1999-07-29
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 255
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-09-618-869-8

Query Match      73.9%; Score 1199; DB 2; Length 236;
Best Local Similarity 96.2%; Pred. No. 6.3e-82;
Matches 227; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 EVKQESGGGLVQPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAISSGSTIY 62
DB 1 DVOLVSSGGGLVQPGGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAISSGSTIY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQTTVTYSSGGGGSG 122
DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQTTVTYSSGGGGSG 120
QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 182
DB 121 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 180
QY 183 KLSGVPARFSGSGGTYSYLTSSMEAEADATYYCQWSSNPLTFGAGTKLEKLR 238
DB 181 KLSGVPARFSGSGGTYSYLTSSMEAEADATYYCQWSSNPLTFGAGTKLEKLR 236

RESULT 4
US-08-956-047-25
/ Sequence 25, Application US/08956047
/ Patent No. 5882924
/ GENERAL INFORMATION:
/ APPLICANT: Fritz, Hans-Joachim
/ APPLICANT: Hennecke, Frank
/ APPLICANT: Kolmar, Harald
/ TITLE OF INVENTION: Genetic Selection, by Means of Signal
/ TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
/ TITLE OF INVENTION: Capable of Ligand Binding
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W., Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/956,047
/ FILING DATE: 22-OCT-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/257,669
/ FILING DATE: 08-JUN-1994
/ APPLICATION NUMBER: DE P 43 19 296.3
/ FILING DATE: 10-JUN-1993
/ CLASSIFICATION: 435
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-63

Query Match 68.0%; Score 1102.5; DB 2; Length 223;
Best Local Similarity 90.3%; Pred. No. 9.1e-75;
Matches 213; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

QY 3 EVKLQSSGGGLVOPGSGSRKLSCAASGFTSSFGMHVROAPEKGLWVAYISSGSSTIY 62
Db 1 DVQLVSSGGGLVOPGSGSRKLSCAASGFTSSFGMHVROAPEKGLWVAYISSGSSTIY 60
QY 63 ADTVKGRFTISRNDPNKNTLFLQMTSLRSEDVVMYICARDYGAYWGQGTITVTVSSGGGGSG 122
Db 61 ADTVKGRFTISRNDPNKNTLFLQMTSLRSEDVVMYICARDYGAYWGQGTITVTVSSGGGGSG 114
QY 123 GGGSGGGSDIELTQSPAIMSASPRVMTWCSSASSVRYMNNFQKSGTSPKRWIYDTS 182
Db 115 -----ASQIVLTQSPAIMSASPGKVTMTWCSSASSVRYMNNFQKSGTSPKRWIYDTS 167
QY 183 KLSSGVPARFSGSGTSYSLTSSMEADAATYYCOOWSSNPLTFGAGTKLEIKR 238
Db 168 KLSSGVPARFSGSGTSYSLTSSMEADAATYYCOOWSSNPLTFGAGTKLEIKR 223

RESULT 6
US-08-564-164A-2
; Sequence 2, Application US/08564164A
; Patent No. 6159947
; GENERAL INFORMATION:
; APPLICANT: Schweighoffer, Fabien
; APPLICANT: Tocque, Bruno
; TITLE OF INVENTION: Intracellular Binding Proteins and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,164A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00714
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93/07241
; FILING DATE: 16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST93030-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3816
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

US-08-564-164A-2

Query Match 59.5%; Score 964.5; DB 3; Length 284;  
Best Local Similarity 72.2%; Pred. No. 2.3e-64;  
Matches 187; Conservative 24; Mismatches 41; Indels 7; Gaps 2;

QY 1 MAEVLQESGGGLVOPGGSRKLSCAASGFTFSFGMHVWROAPEKLEWVAYISSGSSTIY 60  
DB 26 MAQVKLQSGGGLVOPGSRKLSLSCVVSFTFSNGMWRQTPGKLEWVAYISSGSSTIY 85  
QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICAR-----DYGAYWGGTIVTV 114  
DB 86 YYAETVKGRTISRDNKNTLFLQMTSLRSEDVVMYICARHEGTGDTFFDYWGGTIVTV 145  
QY 115 SSGGGGGGGGGGGGGDIETQSPAIMSASPGERVMTCSASSV-RYNNWFOQKSGTS 173  
DB 146 SSGGGGGGGGGGGGGDIETQSPHLSASLGETVSIELASGISTNYLAWYQKPGKS 205  
QY 174 PKRWYDTSKLSSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTK 233  
DB 206 POLLIYVASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYCCQAYKPSFTGAGTK 265  
QY 234 LELKRAAAEOKLISEEDLN 252  
DB 266 LEIKRAAAEOKLISEEDLN 284

## RESULT 7

US-08-190-199A-61  
; Sequence 61, Application US/08190199A  
; Patent No. 5830663  
; GENERAL INFORMATION:  
; APPLICANT: EMBLETON, Michael J.  
; APPLICANT: GOROCIOV, Guy  
; APPLICANT: JONES, Peter T.  
; APPLICANT: WINTER, Gregory P.  
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Microsoft Word  
; CURRENT APPLICATION DATA:  
; FILING DATE: 13-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/01483  
; FILING DATE: 10-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9212419.7  
; FILING DATE: 11-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9117352.6  
; FILING DATE: 10-AUG-1991  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-190-199A-61

Query Match 58.2%; Score 943.5; DB 2; Length 235;  
Best Local Similarity 75.0%; Pred. No. 6.7e-63;

Matches 177; Conservative 26; Mismatches 32; Indels 1; Gaps 1;

QY 3 EVKLQESGGGLVOPGGSRKLSCAASGFTFSFGMHVWROAPEKLEWVAYISSGSSTIY 62  
DB 1 QVQLKESGPGLVAPSQSLISICTVSGFSLTSYGVHWVRQPPGKLEWLVIAWAGGST-NY 59  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYGAWGQTTVTVSAGGGSG 122  
DB 60 NSALMSRLSISKSNKSKQVFLKXNSLQTDITANYICARDRGA YWGQTLVTVSAGGGSG 119  
QY 123 GGGGGGGGGGGGGGGDIETQSPAIMSASPGERVMTCSASSVRYNNWFOQKSGTS 182  
DB 120 GGGGGGGGGGGGGGGDIETQSPAIMSASPGQKVTMTCSASSVSYMHWYQKSGTS 179  
QY 183 KLSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELKR 238  
DB 180 KLASGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELKR 235

## RESULT 8

US-09-423-439-44  
; Sequence 44, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; APPLICANT: BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09423 439  
; FILING DATE: 09-No. 6339070-1999  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-09-423-439-44

Query Match 55.5%; Score 900.5; DB 3; Length 281;  
Best Local Similarity 68.6%; Pred. No. 1.3e-59;  
Matches 179; Conservative 24; Mismatches 43; Indels 15; Gaps 3;

QY 1 MAEVLQESGGGLVOPGGSRKLSCAASGFTFSFGMHVWROAPEKLEWVAYISSGSSTI 60  
DB 21 MAEVLQESGGGLVOPGGSRKLSLSCVVSFTFSNGMWRQTPGKLEWVAYISSGSSTI 80  
QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYIC-----ARDYGAWGQTT 111  
DB 81 YVAPKFRGKATLTADSSNTAYLHLSLTSDTAVYCHVLIYAGYLAWD---YWGQTS 137  
QY 112 VTVSSGGGGGGGGGGGGDIETQSPAIMSASPGERVMTCSASSVRYNNWFOQKSG 171

Db 138 VAVSGGGGGGGGGGGGGQIVLTQSPAIMSASPGKVTITCSASSSVYVMHWFQKPG 197  
Qy 172 TSPKRWIYDTSKLSSGVPARFSGSGTSYSLTISMEADAATYYCQWNSNPLTFGAG 231  
Db 198 TSPKLWYSTNLASGVPARFSGSGTSYSLTISMEADAATYYCQORSTYPLTFGAG 257  
Qy 232 TKLELKRAAEQKLISEEDLN 252  
Db 258 TKLEIKR---EQKLISEEDLN 275

RESULT 9  
US-09-138-091A-76  
; Sequence 76, Application US/09138091A  
; Patent No. 6737249  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: 9491-013-27  
; CURRENT APPLICATION NUMBER: US/09/138,091A  
; CURRENT FILING DATE: 1998-08-21  
; PRIOR APPLICATION NUMBER: US 60/056,736  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE: single chain antibody (scFv) fragments  
; NAME/KEY: VARIANT  
; LOCATION: 208  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-138-091A-76

Query Match 55.3%; Score 897.5; DB 4; Length 245;  
Best Local Similarity 69.8%; Pred. No. 1.9e-59;  
Matches 171; Conservative 34; Mismatches 35; Indels 5; Gaps 2;  
Qy 1 MAEVQLQESGGGLVQPGGSRKLSCAASGFTTSSFGMHVWROAPEKGLWVAYISSGSGTI 60  
Db 1 MAQVLVESGGGLVQPGGSLRLSCLASGFTTSSHHNMVWROAPEKGLWVSISSSSYI 60  
Qy 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYYCARDYGA----YWGQGTITVTVSS 116  
Db 61 YYADSVKGRFTISRDNKNSLYLQWNSLRAEDTAVYYCARDRGSTGMDVWGRGTLTVYSS 120  
Qy 117 GGGSGGGGGGGGSDIELTQSPAIMSASPGERVMTMTCSASSV-RYNNWFQKSGTSPK 175  
Db 121 GGGSGGGGGGGGGSDIQMTQSPSTLSASIGDRVITITCRASEGIYHVLAWYQKPGKAPK 180  
Qy 176 RWIYDTSKLSSGVPARFSGSGTSYSLTISMEADAATYYCQWNSNPLTFGAGTKLE 235  
Db 181 LLIVKASSLASGAPRFGSGSGDTFTXITISLQPDFTATYYCQYSNPLTFGGGTKLE 240  
Qy 236 LKRAA 240  
Db 241 LKRAA 245

RESULT 10  
US-09-192-854-2  
; Sequence 2, Application US/09192854  
; Patent No. 6696245  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides

; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 240  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-2

Query Match 55.1%; Score 894; DB 4; Length 240;  
Best Local Similarity 71.7%; Pred. No. 3.3e-59;  
Matches 172; Conservative 27; Mismatches 37; Indels 4; Gaps 3;  
Qy 3 EVKLQESGGGLVQPGGSRKLSCAASGFTTSSFGMHVWROAPEKGLWVAYISSGSGTYI 62  
Db 1 EVQLLESGGGLVQPGGSLRLSCLASGFTTSSYAMSWVRQAPKGLWVSAISGSGSTYI 60  
Qy 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYYCARDYGA--YWGQGTITVTVSSGGGG 120  
Db 61 ADSVKGRFTISRDNKNSKNTLYLQWNSLRAEDTAVYYCAKSYGAFDYWGQGTITVTVSSGGGG 120  
Qy 121 SGGSGGGGGGS-DIELTQSPAIMSASPGERVMTMTCSASSV-RYNNWFQKSGTSPKRWI 178  
Db 121 SGGSGGGGGGTDIQMTQSPSLASVGDRTVITCRASQSISSLYLWYQKPGKAPKLLI 180  
Qy 179 YDTSKLSSGVPARFSGSGTSYSLTISMEADAATYYCQWNSNPLTFGAGTKLELKR 238  
Db 181 YAASSLQSGVPSRFGSGSGDTFTLITISLQPEDPATYYCQSYSTPNTFGQGTVEIKR 240

RESULT 11  
US-08-918-148-75  
; Sequence 75, Application US/08918148A  
; Patent No. 6342220  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camellia  
; APPLICANT: W.  
; APPLICANT: Carter, Paul J.  
; APPLICANT: Fendly, Brian M.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Agonist Antibodies  
; FILE REFERENCE: P0979  
; CURRENT APPLICATION NUMBER: US/08/918,148A  
; CURRENT FILING DATE: 1997-08-25  
; NUMBER OF SEQ ID NOS: 79  
; SEQ ID NO 75  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: artificial  
US-08-918-148-75

Query Match 54.9%; Score 890.5; DB 3; Length 245;  
Best Local Similarity 69.4%; Pred. No. 6.2e-59;  
Matches 170; Conservative 31; Mismatches 39; Indels 5; Gaps 2;  
Qy 1 MAEVQLQESGGGLVQPGGSRKLSCAASGFTTSSFGMHVWROAPEKGLWVAYISSGSGTI 60  
Db 1 MAEVQLVQSGGGGLVQPGGSLRLSCLASGFTTSDYTMWIRQAPKGLWVSISSGSGTI 60  
Qy 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYYCAR---DYGAYWGQGTITVTVSS 116  
Db 61 YYADSVKGRFTISRDNKNTLYLQWNSLRAEDTAVYYCARWGSBEDAFDIWQGTMTVTVSS 120  
Qy 117 GGGSGGGGGGGGSDIELTQSPAIMSASPGERVMTMTCSASSV-RYNNWFQKSGTSPK 175  
Db 121 GGGSGGGGGGGGSDIVMTQSPSTLSASVGDRTVITCRASEGIYHVLAWYQKPGKAPK 180  
Qy 176 RWIYDTSKLSSGVPARFSGSGTSYSLTISMEADAATYYCQWNSNPLTFGAGTKLE 235





Db	181	LLIYKASSLASCAPSRFSGSGGDTFTLTISLQDDFATYYCQSYNYFLTFGGTKLE	240
Qy	236	LRAA	240
		:	
Db	241	ILRAA	245

RESULT 15

```

RES001 13
US-09/138-091A-74
; Sequence 74, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIORITY APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-09/138-091A-74

```

Query Match	54.3%	Score	881.5	DB	4	Length	245
Best Local Similarity	68.2%	Pred. No.	2.9e-58				
Matches	167	Conservative	33	Mismatches	40	Indels	5
Gaps	2						
QY	1	MAEVLQESGGGLVQPGGSKRLSCAAGFPSSFGMEHWVRQAPKGLWEVAYISGSSTI	60				
DB	1	MAEVQLVQSGGVVQPGGSLSLSCAVSGITLRTYGMHWVRQAPKGLWEVAGISFDGRSE	60				
QY	61	YYADTVKGRFTTISRDNPNKTLFLQMTSLRSEDVTVMYICARDYGAY----	116				
DB	61	YYADSVKGRFTTISRDNKNTLYLQMNLSRAEDTAVYICARDRGSYGMVDMVGRGTMVTIVSS	120				
QY	117	GGGGSGGGGGGGSDIELTQSPAIMASPCERTMTTCSASSV-RVMNFFQOKSGTSPK	175				
DB	121	GGGGSGGGGGGGSDIQLQTSPTLSASTGDRVTITCRASEGIYHWLAWTQQKPGKAPK	180				
QY	176	RWYDTSKLSGVPARFSGSGSGTSYSLTISSSMEAEADAATYVCQWSSNPLTFGAGTKLE	235				
DB	181	LLIYKASSLASAPRSFGSGGDTFTLLSSLOPDDFATYVCOVSNYPLTFGGGTKLE	240				

Search completed: December 30, 2004, 16:04:12  
Job time : 39 secs

**This Page Blank (uspto)**

Query Match	59.1%	Score 959;	DB 15;	Length 291;
Best Local Similarity	70.1%;	Pred. No. 2.5e-57;		
Matches 185;	Conservative 31;	Mismatches 38;	Indels 10;	Gaps 2;
QY	1	MAEVKLQESGGGLVQPGSRKLSCAASGFTFSFGHMHWQAPKGLIEWAYVYSSGSSTI	60	
Db	21	MAQVQLQESGGGVQPSRISLSCAASGFTFSYMSWVRQAPKGLIEWSAISGSGST	80	
QY	61	YYADTVKGRFTISRDNPQNTFLQMTSLRSEDTVMYYCARD-----YGAYWVGQOTT	111	

Db 81 YYADSVKGRFTISRDNSKNTLYIQMNSLRADETALYYCAREGVSSNNWNYFDLWGRGTL 140  
Qy 112 VTVSSGG 170  
Db 141 VTVSSGG 200  
Qy 171 GTSKRWIYDTSKLSGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGA 230  
Db 201 GRAPKLLIYAASLQGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGA 260  
Qy 231 GTKLEKRAAAEQKLISEEDLNGA 254  
Db 261 GTKLEKRAAAEQKLISEEDLNGA 284

RESULT 2  
US-09-818-247-22  
; Sequence 22, Application US/09818247  
; Patent No. US20020102657A1  
; GENERAL INFORMATION:  
; APPLICANT: Mostov, Keith E.  
; APPLICANT: Richman-Eisenstat, Janice  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,  
; FILE REFERENCE: 18062E-000910US  
; CURRENT APPLICATION NUMBER: US/09/818,247  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: WO PCT/US01/09699  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/192,197  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 60/192,198  
; PRIOR FILING DATE: 2000-03-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence: Pelb/4AF/myc/6His  
US-09-818-247-22

Query Match 58.2%; Score 943.5; DB 9; Length 288;  
Best Local Similarity 69.3%; Pred. No. 2.8e-56;  
Matches 181; Conservative 32; Mismatches 41; Indels 7; Gaps 2;  
Qy 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTI 60  
Db 21 MAQVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVAVISSGGST 80  
Qy 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYICARD-----YGAYWQGGTTV 114  
Db 81 YYADSVKGRFTISRDNKNTLYIQMNSLRADETAVYCARSTVNSGYFQHWGQGLTVTV 140  
Qy 115 SSGGG 173  
Db 141 SSGGG 200  
Qy 174 PKRWIYDTSKLSGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGAGTK 233  
Db 201 PKLLIYKASSLASGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGAGTK 260  
Qy 234 LELKRAAAEQKLISEEDLNGA 254  
Db 261 VDIKRAAAEQKLISEEDLNGA 281

RESULT 3  
US-10-406-830-9

; Sequence 9, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 9  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-9

Query Match 57.2%; Score 927; DB 15; Length 291;  
Best Local Similarity 67.4%; Pred. No. 3.7e-55;  
Matches 178; Conservative 36; Mismatches 40; Indels 10; Gaps 2;  
Qy 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAVISSGSTI 60  
Db 21 MAQVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVAVISSGGST 80  
Qy 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYICARD-----YGAYWQGGTT 111  
Db 81 YYADSVKGRFTISRDNKNTLYIQMNSLRADETAVYCARSTVNSGYFQHWGQGLTVTV 140  
Qy 112 VTVSSGG 170  
Db 141 VTVSSGG 200  
Qy 171 GTSKRWIYDTSKLSGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGA 230  
Db 201 GRAPKLLIYAASLQGVVPARESGSGSTYSYSLTSSMEAEADATYYCQWSSNPLTFGA 260  
Qy 231 GTKLEKRAAAEQKLISEEDLNGA 254  
Db 261 GTKLEKRAAAEQKLISEEDLNGA 284

RESULT 4  
US-10-406-830-5  
; Sequence 5, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406,830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent In version 3.2  
; SEQ ID NO 5  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-5

## US-10-406-830-5

Query Match	57.1%	Score 926;	DB 15;	Length 287;
Best Local Similarity	69.6%;	Pred. No. 4.3e-55;		
Matches 181;	Conservative 32;	Mismatches 41;	Indels 6;	Gaps 3
Qy 1	MAEVLQESGGGLVOPGSRKLSCAAAGFTTSSFGMHVVRQAPKGLWVAYISGSSTI	60		
Db 21	MAQVLVESGGGVVQGRSLRSLCAAAGFTTSDYYIHVVRQAPKGLWMAVISYDGNKK	80		
Qy 61	YYADTVAGRFITSRDNPQNTLFLQWTSLSRSDTVMYYICARD-YG---AYAGQGQTTVTS	115		
Db 81	YYAASVKDRFTISRDNKNVTSLQWNSLRADTAVVYCARDLYGDYALDYQGQTLVTS	140		
Qy 116	SGGGGGGGGGGGSDIELTQSPALMSASPGERVMTTCSSSV-RYMNWFQOKSGTSP	174		
Db 141	SGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVITITCRASQSGTSLWAWYQKPKGAP	200		
Qy 175	KRWLYDTSKLSSGVPARPFGSGSGTYSYSLTISSEAEADAANYTCQWSSNPITFCAGNKL	234		
Db 201	KLLIYKASTLESQVPSRFTSGSGTGTEFTLTISGLQDFATYYCQKSSYPLTFGGGTVK	260		
Qy 235	ELKPAAAEQKLISEDLNGA	254		
Db 261	EIKKAAAEOKLISEDLNGA	280		

## RESULT 5

```

US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Qu, Shimian
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259,087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

```

## Query Match

Query Match	56.3%	Score 913;	DB 14;	Length 242;
Best Local Similarity	71.1%;	Pred. No. 2.7e-54;		
Matches 172;	Conservative 30;	Mismatches 36;	Indels 4;	Gaps 2;
QY	1	MAEVKLQESGGGLVQPGGSRKLSCAAAGFTFSSFGMEHWVROAPEKGLEWVAIYSSGSGSTI	60	
DB	1	MAQVKLQGSPELVKPAASVWMSKASGTTFTSMHWVKOKPQCGLEWIGYINPYNDGT	60	
QY	61	YYADTVKGRFTISRDNPKNTLFLQWTSLRSEDVTVMYCAR--DYCA--YWGQGTTVTVSS	116	
DB	61	KYNEKPKGAALTSDDKSSSTAYMELSLTSDSAVYYCAREGNYGALDYMCGQGTTVTVSS	120	
QY	117	GGGGSGGGGGGGSDIELTQSPAIMASPGERTVMTCSASSSVRYMNVFOOKSGTSPKP	176	
DB	121	GGGGSGGGGGGGSDIELTQSPITMGASPGKEVTTTCSASSSVYMHVFOOKPGTSPKP	180	
QY	177	WIYDTSKLSSGVPARFSGSGSGTSTYSLTISMEAEADAATYYCQOWSSNPLTFGAGTKLEL	236	
DB	181	WIYGTSLNLAGVPVRFSGSGSGTSYSTISMEAEADAATYYCQOWSSYPLTFGGGTKLEI	240	
QY	237	KR 238		

D<sub>b</sub> 241 KR 242

RESULT 6  
 US-10-689-006-20  
   Sequence 20, Application US/10689006  
   Publication No. US20040191249A1  
   GENERAL INFORMATION:  
   APPLICANT: Vanderbilt University  
   APPLICANT: Hallahan, Dennis E  
   APPLICANT: Mernaugh, Raymond  
   TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS  
   FILE REFERENCE: 1242/72  
   CURRENT APPLICATION NUMBER: US/10/689,006  
   CURRENT FILING DATE: 2003-10-20  
   PRIOR APPLICATION NUMBER: US 09/914,605  
   PRIOR FILING DATE: 2001-08-30  
   PRIOR APPLICATION NUMBER: US 10/259,087  
   PRIOR FILING DATE: 2002-09-27  
   NUMBER OF SEQ ID NOS: 34  
   SOFTWARE: PatentIn version 3.2  
   SEQ ID NO 20  
   LENGTH: 242  
   TYPE: PRT  
   ORGANISM: Artificial  
   FEATURE:  
   OTHER INFORMATION: Artificial antibody ligand number 2  
 US-10-689-006-20

Query Match 56.3%; Score 913; DB 17; Length 242;  
Best Local Similarity 71.1%; Pred. No. 2.7e-54;  
Matches 172; Conservative 30; Mismatches 36; Indels

Qy	1	MAEVKLOBSGGGLVOPGSGSRKLSCKASGFTFSSFGMHVWROAPEKGLIEWAYISSGSGSTI	60
Db	1	MAQVKLQOSGPELVKRPFGASVKMSCKASGYTFTSYVMEHWVKQPKQOGLIEWTGINPYNDGT	60
Qy	61	YYADTVKGRFTISLRDNPKNTLFLQWLTSLRSDDTVMYICAR--DYGA--YVQOGGTTVTVSS	116
Db	61	KYNEKFKKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYGALDYGQGGTTVTVSS	120
Qy	117	GGGGGGGGGGGGGGDIELTQSPALMSASPERVTMTCSASSSVRYNNWFQOQSGTSPKR	176
Db	121	GGGGGGGGGGGGGGDIELTQSPITMSASPEKVTITCSASSSVSYMHWFKQKPGTSPKP	180
Qy	177	WYIDTKLSGGVPARFSGSGGTGTSYSLTISMEAEADAATYYCQOQSSNPILTFGAGTKLEL	236
Db	181	WYIGTINLASGVVPFRFSGSGGTGTSYSLTISMEAEADAATYYCQOQSSYPLTFGGGTKLEI	240
Qy	237	KR 238	
Db	241	KR 242	

## RESIT.T 7

```

RES001 7
US-09-880-748-2104
; Sequence 2104, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

```

```
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2104
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2104

Query Match      55.9%; Score 906.5; DB 10; Length 237;
Best Local Similarity 72.6%; Pred. No. 7.4e-54;
Matches 172; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVROAPEKGLEWVAYISGSGSTIYY 62
DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNWVRQAPGKLEWVSISGSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWGQGTITVTVSSGGGSG 122
DB 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDTDDYWGQGTITVTVSSGGGSG 120

QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTVITCRASQGISSSLAWYQKPGRAPKVLIIYA 180

QY 182 SKLSSGVPAFRFSGSGSTSYSLTISMEAEADAATYYCQWSSNPLTFGAGTKLELKR 238
DB 181 STLESGVPSRFSGSGGTDFLTITSLQPEDFATYYCQSYSTPWTFGQGTKEIKR 237

RESULT 8
US-10-293-418-2104
; Sequence 2104, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2104
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2104

Query Match      55.9%; Score 906.5; DB 14; Length 237;
Best Local Similarity 72.6%; Pred. No. 7.4e-54;
Matches 172; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVROAPEKGLEWVAYISGSGSTIYY 62
DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNWVRQAPGKLEWVSISGSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWGQGTITVTVSSGGGSG 122
DB 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDTDDYWGQGTITVTVSSGGGSG 120

QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTVITCRASQGISSSLAWYQKPGRAPKVLIIYA 180

QY 182 SKLSSGVPAFRFSGSGSTSYSLTISMEAEADAATYYCQWSSNPLTFGAGTKLELKR 238
DB 181 STLESGVPSRFSGSGGTDFLTITSLQPEDFATYYCQSYSTPWTFGQGTKEIKR 237

RESULT 9
US-09-880-748-2020
; Sequence 2020, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2020
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2020

Query Match      55.7%; Score 903.5; DB 10; Length 237;
Best Local Similarity 72.6%; Pred. No. 1.2e-53;
Matches 172; Conservative 27; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGHWHVROAPEKGLEWVAYISGSGSTIYY 62
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNWVRQAPGKLEWVSISGSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGYWGQGTITVTVSSGGGSG 122
DB 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARDTDDYWGQGTITVTVSSGGGSG 120

QY 123 GGGSGGGSDIELTQSPAIMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTVITCRASQGISSSLAWYQKPGRAPKVLIIYA 180

QY 182 SKLSSGVPAFRFSGSGSTSYSLTISMEAEADAATYYCQWSSNPLTFGAGTKLELKR 238
DB 181 STLESGVPSRFSGSGGTDFLTITSLQPEDFATYYCQSYSTPWTFGQGTKEIKR 237

RESULT 10
US-10-293-418-2020
; Sequence 2020, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
```

Query Match 55.7%; Score 903.5; DB 14; Length 237;  
Best Local Similarity 72.6%; Pred. No. 1.2e-53;  
Matches 172; Conservative 27; Mismatches 37; Indels 1; Gaps 1;  
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSGSTIYY 62  
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYMNWVRQAPKGLWVSISSGSGSTIYY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGTITVTSSGGGSG 122  
DB 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGLTIVTSSGGGSG 120  
QY 123 GGGSGGGSDIELTQSPAIMSASPCRVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181  
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGRAKVLIIYA 180  
QY 182 SKLSSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238  
DB 181 STLESVPSPRFSFGSGSGTDFLTITSSLPQDFATYCCQSYSTPTWTFQGQTKLEIKR 237  
; PRIORITY: 237  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2005  
Query Match 55.7%; Score 903.5; DB 14; Length 237;  
Best Local Similarity 72.6%; Pred. No. 1.2e-53;  
Matches 172; Conservative 27; Mismatches 37; Indels 1; Gaps 1;  
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSGSTIYY 62  
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYMNWVRQAPKGLWVSISSGSGSTIYY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGTITVTSSGGGSG 122  
DB 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGLTIVTSSGGGSG 120  
QY 123 GGGSGGGSDIELTQSPAIMSASPCRVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181  
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGRAKVLIIYA 180  
QY 182 SKLSSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238  
DB 181 STLESVPSPRFSFGSGSGTDFLTITSSLPQDFATYCCQSYSTPTWTFQGQTKLEIKR 237

RESULT 11  
US-09-880-748-2005  
; Sequence 2005, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2005  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2005  
Query Match 55.5%; Score 900.5; DB 10; Length 237;  
Best Local Similarity 72.2%; Pred. No. 1.9e-53;  
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;  
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSGSTIYY 62  
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYMNWVRQAPKGLWVSISSGSGSTIYY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGTITVTSSGGGSG 122  
DB 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGLTIVTSSGGGSG 120  
QY 123 GGGSGGGSDIELTQSPAIMSASPCRVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181  
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGRAKVLIIYA 180  
QY 182 SKLSSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238  
DB 181 STLESVPSPRFSFGSGSGTDFLTITSSLPQDFATYCCQSYSTPTWTFQGQTKLEIKR 237

RESULT 12  
US-09-880-748-2114  
; Sequence 2114, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2114  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2114  
Query Match 55.5%; Score 900.5; DB 10; Length 237;  
Best Local Similarity 72.2%; Pred. No. 1.9e-53;  
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;  
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSGSTIYY 62  
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYMNWVRQAPKGLWVSISSGSGSTIYY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWQGTITVTSSGGGSG 122  
DB 61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYICARDTDDYWGQGLTIVTSSGGGSG 120  
QY 123 GGGSGGGSDIELTQSPAIMSASPCRVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181  
DB 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGRAKVLIIYA 180  
QY 182 SKLSSGVPARFSGSGSGTSYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238  
DB 181 STLESVPSPRFSFGSGSGTDFLTITSSLPQDFATYCCQSYSTPTWTFQGQTKLEIKR 237

RESULT 13  
US-10-293-418-2005  
; Sequence 2005, Application US/10293418  
; Publication No. US20030223996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2005  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2005  
Query Match 55.5%; Score 900.5; DB 10; Length 237;  
Best Local Similarity 72.2%; Pred. No. 1.9e-53;  
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;





Db 181 STLESGVPSRFGSGGTDFTLTISLQPEDFATYYCQSYSTPWTFFGQTKLEIKR 237

Search completed: December 30, 2004, 16:07:11  
Job time : 143 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:46:06 ; Search time 40 Seconds  
(without alignments)  
760.112 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVKLOBSGGGLVOPGSR.....VLTITSLIILMLWQKKPR 316  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 164529

Minimum DB seq length: 0  
Maximum DB seq length: 316

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	892.5	55.0	268	2 A56446	Ig heavy chain V r
2	718.5	44.3	249	2 S41374	single chain Fv an
3	626.5	38.6	233	2 JCS322	p53 specific singl
4	555.5	34.2	213	2 S68213	Ig heavy chain (Ma
5	535	33.0	136	1 GIMS21	Ig heavy chain pre
6	522.5	32.2	121	2 B34871	Ig heavy chain V r
7	516	31.8	130	1 JL0079	Ig kappa chain pre
8	514	31.7	235	2 S25058	Ig kappa chain - m
9	511	31.5	107	2 A30562	Ig kappa chain V r
10	508	31.3	103	2 S29591	Ig kappa chain V r
11	508	31.3	104	2 B49049	Ig kappa chain V r
12	506	31.2	106	2 P30071	Ig kappa chain V r
13	506	31.2	107	2 B30562	Ig kappa chain V r
14	501	30.9	107	2 S11118	Ig kappa chain V r
15	498	30.7	107	2 S11119	Ig kappa chain V r
16	498	30.7	107	2 PC4405	Ig kappa chain V r
17	490	30.2	107	2 S11121	Ig kappa chain V r
18	488	30.1	107	2 PT0406	Ig kappa chain V r
19	484.5	29.9	143	2 S23624	Ig heavy chain V r
20	483	29.8	107	2 S11117	Ig kappa chain V r
21	482	29.7	120	2 S12953	Ig heavy chain V r
22	481.5	29.7	108	2 G30560	Ig kappa chain V r
23	480	29.6	94	2 D25913	Ig heavy chain V r
24	479	29.5	100	2 S29590	Ig kappa chain V r
25	478	29.5	107	2 S11112	Ig kappa chain V r
26	478	29.5	108	2 PH1015	Ig heavy chain V r
27	476	29.3	107	2 PD0011	Ig kappa chain V r
28	473	29.2	97	2 PH1084	Ig light chain V r
29	473	29.2	114	2 S46392	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A>Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:CROSS-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 892.5; DB 2; Length 268;  
Best Local Similarity 65.9%; Pred. No. 1.2e-52;  
Matches 176; Conservative 26; Mismatches 52; Indels 13; Gaps 2;  
Qy 1 MAEVKLOBSGGGLVOPGSRKLSCAAGTFTSSFGMHVROAPKGLWVAYISGSGSTI 60  
Db 1 MAQVKLOESGAELVKPGASVKLSCTTSFGNFKDTYHMKVQRPQGLEWIGRIAPANGIT 60  
Qy 61 YYADTVKGRFTISRDNPKNLTFLQWTSLSRSEDTWYYCA----RDYGYWGGGTTVTYSS 116  
Db 61 KYDPKFGQKATIAADTSNTAYLQLSLTSDTAVYYCASYLTTRYENWGGGTTVTYSS 120  
Qy 117 GGGSGGGSGGGGGSDIELTQSPAIMSASPCRVTMTCSASSSVRYMNFQOKSGTSPKR 176  
Db 121 GGGSGGGSDSGGGSDIELTQSPAIMSASLGEKVTMCRASSSVNFIWYQOKSDASPKL 180  
Qy 177 WIYDTSKSSGVPARFSGSGSGTSYSLTISMEADATYYCQOWSNPLFTFGAGTKLEL 236  
Db 181 WVYVTSHPGPVAPFSGSGSGSYSLTISMEGDAATYYCQQTSPFTFGSGTKLEI 240  
Qy 237 KRA-----AAEQKLISEEDLNGA 254  
Db 241 KRSAHHHHHHGAAEQKLISEEDLNGA 267

RESULT 2

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv antibody  
A:Reference number: S41374

```
A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:229480

Query Match      44.3%; Score 718.5; DB 2; Length 249;
Best Local Similarity 57.8%; Pred. No. 4.7e-41;
Matches 144; Conservative 31; Mismatches 63; Indels 11; Gaps 3;

QY 3 EVKLOSGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSSIIY 62
Db 1 QVQLQSGAELVPGASVKLSCTASGFNPKDIIHWKQPEKGLWVAYISGSSIIY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDY---YGA--YWGQGTIVTVSSG 117
Db 61 VPRFQDKATITADTSNTAYLSSLTSEDVAVYICARRDLYTSLGYWGQGTIVTVSSR 120

QY 118 GGGSGGGGGGGGSDIELTQSPAIMSASGPERVTWTCSSASSV-----RYMWNFQOKSG 171
Db 121 GGGSGGGGGGGGSDIELTQSPVSVVIFGSEVSISCRSSKLLYSDGDSLFWFLQRP 180

QY 172 TSPKRWIYDTKSLSGVPAFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAG 231
Db 181 QSPQLLIYRMSNLASGVPDRFSGSGGTSFTLRISRAEADVGVYICQHQREYPLTFGAG 240

QY 232 TKLELKRAA 240
Db 241 TKLELKRAA 249

RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydriocloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match      38.6%; Score 626.5; DB 2; Length 233;
Best Local Similarity 55.3%; Pred. No. 6.1e-35;
Matches 131; Conservative 29; Mismatches 66; Indels 11; Gaps 5;

QY 7 QESGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYI--SSGSSIIYAD 64
Db 1 QESGAELVRSASVKLSCTTSGFNINDYMHWKRPQGLEWIGRIDPENGADWTRSS 60

QY 65 TVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDYGAIWGQGTIVTVSSGGSGGG 124
Db 61 GVKA--TMTADTSNTAYLQLSLTSEDVAVYICNAGMD-YWGQGTIVTVSSGGSGGR 117

QY 125 GSGGGGSDIELTQSPAIMSASGPERVTWTCSSASSV-----RYMWNFQOKSGTSPKRWIY 179
Db 118 ASGGGGSDIELTQSPASVLSGORATISCRASVSTSGSYMHWNQKQPGPPRLIY 177

QY 180 DTSKLSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLEL 236
Db 178 LVSNLSEGVPAFSGSGGTDFTLNTHPVEEADAATYICQHIHRELTRSEG-GTKLEI 233

RESULT 4
S68213
Ig heavy chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
```

```
C;Accession: S68213
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68213
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-213 <TAK>
A;Cross-references: UNIPROT:Q91Z05; EMBL:D29667
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IMM>

Query Match      34.2%; Score 555.5; DB 2; Length 213;
Best Local Similarity 53.9%; Pred. No. 3.1e-30;
Matches 124; Conservative 17; Mismatches 50; Indels 39; Gaps 5;

QY 4 VKLQESGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSSIIY 63
Db 2 VQLVESGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSSIIY 61

QY 64 DTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARDY---GAYWGQGTIVTVSSGGG 120
Db 62 DTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYICARSWLLPFDYWGQGTITLVSSA--- 118

QY 121 SGGGGGGGGSDIELTQSPAIMSASGPERVTWTCSSASSVRYMWNFQOKSGTSPKRWIY 180
Db 119 -----KTPPSVYPLAPGCGDTTGGSSVTGLCVKGYFPESVTVT-----WN 159

QY 181 TSKLSSGV---PARTFSGSGGTSYSLTISSEAEADAATYICQWSSNPLT 227
Db 160 SGLSSSVHTFALQSGLYTWSSSVTVPS-----STWPSQTVT 198

RESULT 5
G1MS21
Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: E90809; A93184; A02066
R;Bothwell, A.L.M.; Paekind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some
A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: E90809
A;Molecule type: mRNA
A;Residues: 1-136 <BOT>
A;Cross-references: UNIPROT:P01783; GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055
R;Adetugbo, K.; Milstein, C.; Secher, D.S.
Nature 265, 299-304, 1977
A;Title: Molecular analysis of spontaneous somatic mutants.
A;Reference number: A93184; MUID:77100368; PMID:401950
A;Contents: myeloma protein MOPC 21
A;Accession: A93184
A;Molecule type: protein
A;Residues: 1-74, 'D', 76-77, 'H', 79-88, 'ND', 91-114, 'H', 116-119, 'W', 121-136 <ADE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
F;31-114/Domain: immunoglobulin homology <IMM>
F;115-119/Region: D segment
F;120-136/Region: J segment
F;38-112/Disulfide bonds: #status experimental

Query Match      33.0%; Score 535; DB 1; Length 136;
Best Local Similarity 87.5%; Pred. No. 4.4e-29;
Matches 105; Conservative 5; Mismatches 4; Indels 6; Gaps 2;

QY 3 EVKLOSGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSSIIY 62
Db 17 DVQLVESGGGLVQPGGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSSIIY 76
```

A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional sequences extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)

C;Genetics:

A;Gene: V(kappa)Ox1

A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology

C;Superfamily: heterotetramer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>

F;38-111/Domain: immunoglobulin homology <IMM>

F;45-109/Disulfide bonds: #status predicted

Query Match 31.8%; Score 516; DB 1; Length 130;  
Best Local Similarity 92.5%; Pred.No. 7.8e-28;  
Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPERVTMTCSASSSVRYMMWFQKSGTSPKRWIYDTSKLSSGVGPARF 192  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 24 IVLTQSPAIMSASPERVKTMTCSASSSVSYMYWYQQKSGTSPKRWIYDTSKLSSGVGPARF 83  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 193 SGSGSGTSYSLTISSMEAEADATYYCQOWSSNPLTFGAGTKLELKRRA 239  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 84 SGSGSGTSYSLTISSMEAEADATYYCQOWSSNPLTFGAGTKLELKRRA 130  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8

S25058

Ig kappa chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

R;Accession: S25058

R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992

A;Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific antigen

A;Reference number: S25057

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-235 <PIS>

A;Cross-references: EMBL:X67211; NID:G54828; PIDN:CAM47650.1; PID:G54829

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;38-111/Domain: immunoglobulin homology <IMM>

Query Match 31.7%; Score 514; DB 2; Length 235;  
Best Local Similarity 91.7%; Pred.No. 2e-27;  
Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPERVTMTCSASSSVRYMMWFQKSGTSPKRWIYDTSKLSSGVGPARF 192  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 24 IVLTQSPAIMSASPERVKTMTCSASSSVSKMWYQQKSGTSPKRWIYDTSKLSSGVGGRF 83  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 193 SGSGSGTSYSLTISSMEAEADATYYCQOWSSNPLTFGAGTKLELKRRAA 241  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 84 SGSGSGTSYSLTISSMEAEADATYYCQOWSSNPLTFGAGTKLELKRADA 132  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9

A30562

Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000

C;Accession: A30562

R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
J. Immunol. 142, 888-893, 1989

A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site

A;Reference number: A30562; MUID:89110066; PMID:2464031

A;Accession: A30562

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-107 <SIK>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.5%; Score 511; DB 2; Length 107;  
Best Local Similarity 91.5%; Pred. No. 1.4e-27;  
Matches 97; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192  
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPARF 61  
QY 193 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEKR 238  
Db 62 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLYFGGTKLEIKR 107

## RESULT 10

S29591  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S29591  
R;Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A;Reference number: S26459  
A;Accession: S29591  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-103 <AV>  
A;Cross-references: EMBL:X59094; NID:g52227; PID:CAA41820.1; PID:g52228  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 103;  
Best Local Similarity 94.2%; Pred. No. 2.1e-27;  
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192  
Db 1 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPARF 60  
QY 193 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLE 235  
Db 61 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLE 103

## RESULT 11

B49049  
Ig kappa chain V region (anti-idiotypic) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B49049  
R;Akmandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.  
Eur. J. Immunol. 22, 2893-2899, 1992  
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen  
A;Reference number: A49049; MUID:93049629; PMID:1425914  
A;Accession: B49049  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-104 <ARM>  
A;Experimental source: BALB/c  
A;Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIPI:118299)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 104;  
Best Local Similarity 94.2%; Pred. No. 2.1e-27;  
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192  
Db 1 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPARF 60

Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPARF 61  
QY 193 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLE 235  
Db 62 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLE 104

## RESULT 12

PS0071  
Ig kappa chain V region (38C13.V8) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: PS0071  
R;Levy, S.; Campbell, M.J.; Levy, R.  
J. Exp. Med. 170, 1-13, 1989  
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement  
A;Reference number: A92781; MUID:89310348; PMID:2501443  
A;Accession: PS0071  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <LEV>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 106;  
Best Local Similarity 92.4%; Pred. No. 2.9e-27;  
Matches 97; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192  
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEK 237  
Db 62 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEK 106

## RESULT 13

B30562  
Ig kappa chain V region (27.10.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C;Accession: B30562  
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L  
J. Immunol. 142, 888-893, 1989  
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding  
A;Reference number: A30562; MUID:89110066; PMID:2464031  
A;Accession: B30562  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <SIK>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 107;  
Best Local Similarity 89.6%; Pred. No. 3e-27;  
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSSGVPARF 192  
Db 2 IVLTQSPAIMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSSGVPTRF 61

QY 193 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLTFGAGTKLEKR 238  
Db 62 SSGSGTYSYSLTSSMEADAATYYCQWSSNPLYFGGTKLEIKR 107

## RESULT 14

S11118  
Ig kappa chain V region (clone N05-61.1.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)

Search completed: December 30, 2004, 15:55:36  
Job time : 42 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:38:05 ; Search time 188 Seconds  
(without alignments)  
967.119 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVLQBSGGGLVQPGGSR.....VLTITISLILMLQKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1144693

Minimum DB seq length: 0  
Maximum DB seq length: 316

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	853.5	52.6	298	2 Q9QYF0	Q9qyf0 synthetic c
2	850	52.4	255	2 Q6KB05	Q6kb05 mus musculus
3	850	52.4	255	2 Cag34081	Cag34081 mus muscu
4	695	42.8	241	2 Q921A6	Q921a6 mus musculus
5	658	40.6	243	2 Q7TQM2	Q7tcqm2 mus musculus
6	608.5	37.5	218	2 Q925S1	Q925s1 mus musculus
7	535	33.0	136	1 HV16_MOUSE	P01783 mus musculus
8	507	31.3	107	1 KV6F_MOUSE	P04940 mus musculus
9	506	31.2	107	1 KV6H_MOUSE	P04942 mus musculus
10	502	30.9	107	1 KV6I_MOUSE	P04943 mus musculus
11	500	30.8	107	1 KV6G_MOUSE	P04941 mus musculus
12	498	30.7	112	2 Q8KIF0	Q8kif0 mus musculus
13	494	30.5	107	1 KV6J_MOUSE	P04944 mus musculus
14	491	30.3	235	2 Q91W12	Q91w12 mus musculus
15	483	29.8	134	2 ORVDD0	Q8vdd0 mus musculus
16	480	29.6	112	2 Q8KIF2	Q8kif2 mus musculus
17	462.5	28.5	113	2 Q9UL90	Q9ul90 homo sapien
18	461	28.4	112	2 Q8KIF3	Q8kif3 mus musculus
19	458	28.2	111	2 AAR10981	Aar10981 mus muscu
20	458	28.2	111	2 AAR10982	Aar10982 mus muscu
21	458	28.2	114	2 Q8KIF1	Q8kif1 mus musculus
22	457	28.2	108	2 AAR11048	Aar11048 mus muscu
23	453	27.9	92	2 AAR11066	Aar11066 mus muscu
24	452.5	27.9	119	2 Q920E7	Q920e7 mus musculus
25	450.5	27.8	128	2 BAD00406	Bad00406 camelus d
26	447	27.6	110	2 AAR10999	Aar10999 mus muscu
27	447	27.6	121	2 BAD00469	Bad00469 camelus d
28	446.5	27.5	119	2 AAL35865	Aal35865 lama glam
29	446	27.5	107	1 KV6C_MOUSE	P01677 mus musculus
30	446	27.5	124	2 BAD00233	Bad00233 camelus d
31	445.5	27.5	117	2 AAL35877	Aal35877 lama glam

32	445	27.4	118	2 Q9UL91	Q9ul91 homo sapien
33	443	27.3	119	2 BAD00422	Bad00422 camelus d
34	442.5	27.3	126	2 BAD00440	Bad00440 camelus d
35	441	27.2	107	1 KV6B_MOUSE	P01676 mus musculus
36	440.5	27.2	116	2 Q9UL93	Q9ul93 homo sapien
37	440	27.1	107	1 KV6D_MOUSE	P01678 mus musculus
38	439	27.1	119	2 BAD00492	Bad00492 camelus d
39	438.5	27.0	123	2 BAD00234	Bad00234 camelus d
40	438.5	27.0	124	2 BAD00534	Bad00534 camelus d
41	438.5	27.0	128	2 BAD00444	Bad00444 camelus d
42	438.5	27.0	131	2 Q811C3	Q811c3 mus musculus
43	438	27.0	118	2 AAL35882	Aal35882 lama glam
44	437.5	27.0	126	2 BAD00510	Bad00510 camelus d
45	437	26.9	106	2 Q9U410	Q9u410 schistosoma

ALIGNMENTS

RESULT 1  
Q9QYF0 PRELIMINARY; PRT; 298 AA.  
AC Q9QYF0;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE CN 8 single chain antibody.  
GN Name=CN 8 scFv;  
OS synthetic construct.  
OC artificial sequences.  
OX NCBI\_TaxID=32630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20183931; PubMed=10706631;  
RA Shinohara N.; Demura T.; Fukuda H.;  
RT "Isolation of a vascular cell wall-specific monoclonal antibody  
RT recognizing a cell polarity by using a phase display subtraction  
RT method.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).  
DR EMBL; AB036341; BAA88633.1; -.  
DR PIR; A33933; A33933.  
DR PIR; S19112; S19112.  
DR HSSP; P01820; 1A70.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match	52.6%;	Score 853.5;	DB 2;	Length 298;
Best Local Similarity	66.3%;	Pred. No. 3.2e-54;		
Matches 163;	Conservative 32;	Mismatches 46;	Indels 5;	Gaps 2;
QY	1	MAEVLQBSGGGLVQPGGSRKLSCAAGSFTFSFGMHVVRQAPKGLWVAYISGSSTI	60	
Db	38	MAQVKLQSGGGLVKPGGSLKLSCAASGDSFYWMVMVRQAPGKGLWGEINPDSSTI	97	
QY	61	YYADTVKGRFTISRDNPANTLFLQMTSLRSDTVNYICAR-----DYGAYWGGTITVTYSS	116	
Db	98	NYTPSLKDKFTISRDNKNTLYLQMSKVRSEDTALYYCARASYIGHSAYWGQTTVTYSS	157	
QY	117	GGGSGGGGGGGSDIELTOSPAIMSAPCERVMTCSASSV-RYMNWFQKSGTSPK	175	
Db	158	GGGSGGGGGGGGGSDIELTOSPASLSASVGETVTITCRASGNHNYLAWTQQKQKSPQ	217	
QY	176	RWYIDTKLTSVGPVRFSGSGSGTYSYLITISSEAEADAATYYCQWSSNPITFGAGTKLE	235	
Db	218	LLVTNXTLADGVSRFSFGSGSGTQYSLKNSLQPEDFGSYCQHFHTPTPTFGGGTKLE	277	
QY	236	LKRAAA 241		
Db	278	IKRAAA 283		

RESULT 2
Q6KB05 PRELIMINARY; PRT, 255 AA.
ID Q6KB05
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv_B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -
DR InterPro; IPR0031599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR0031596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SMO0409; IG; 2.
DR PROSITE; PS00406; IGv; 2.
FT NON TER
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
Query Match 52.4%; Score 850; DB 2; Length 255;
Best Local Similarity 67.1%; Pred. No. 4.8e-54;
Matches 167; Conservative 29; Mismatches 39; Indels 14; Gaps 4;
QY 3 EVKLQESGGGLVPQGSRKLSAASGTFSSFGMHVWROAPEKGLEWVAIVSGSSTIYY 62
Dd 1 QVLQLQQSGDLVKPGSLKVSAAASGTFSSYGMSWRQTDPDKLEWVAITISGGSYTY 60
QY 63 ADTVKGRFTISRDNPKNTLFLOMTSLRSETVMYCAR--DY---GA--YMGGGTVTVS 115
Dd 61 PDSVKGRFTISRDNAPKNTLYLQMSLSKSEDTAMYICARHINRYDGFADYMGCGTTLTVS 120
QY 116 SGCGSGSGSGSGSGSDIELTSQPAIMSAPGERVTWTCSASSSV-----RYMNHFFQ 168
Dd 121 SGCGSGSGSGSGSGSDLVMAQSPLSVSAGEKVIMSCKSQSILNSRNKNVIAMTQQ 180
QY 169 KSGTSPKRWIYDTKLSSGVPAFPSSGSGTSTSYLSISSMEADAATYYCOOWSNPLTF 228
Dd 181 KPQGSFKLLIYGATRSGVDPRPTSGSGGTDFLTIISSVQAEDIAVYCONDHSHYLTF 240
QY 229 GAGTKLELK 237
Dd 241 GAGTKLEIK 249
RESULT 3
CAG34081 PRELIMINARY; PRT, 255 AA.
ID CAG34081
AC CAG34081;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN SCFv B8E5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=balb/c;

```
QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTIYY 62
Db 1 QVKLQSGGPELKKPGETVKISCKASGYTFTDYGNNWVKQAPKGLKMWGINTYGEPTY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYYCARD---YGAHWGQGTVTYVSSGG 118
Db 61 ADDFKRFAFSLTSASTAYLQINLKNEDTATYFCARKDLLRYPDYWGQGTVTYVSSGG 120

QY 119 GSGGGGGGGGGSDIELTQSPAIMSAPGERVTMTCSASSV-RYMNWFOQKSGTSPKR- 176
Db 121 GSGGGGGGGGGSDIELTQSPSSLSASLGKVTITCKASQDINKYIAWYQKPGKPRSA 180

QY 177 ---WYDTSKLSSGVPARFSGSGTGYSLTISMEADAATYYCQWSSNPLTFAGTK 233
Db 181 HTLHIY----IQPGIPSRFSGSGRSDYFSFSLNLEPDIAITYCLHY-DNLHTFGGGTK 235

QY 234 LELKRA 239
Db 236 LELKRA 241

RESULT 5
Q7TQM2 PRELIMINARY; PRT; 243 AA.
ID Q7TQM2
AC Q7TQM2
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE scFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX Peter J.C., Eftekhari P., Billiard P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER
FT 1
FT 1
SQ SEQUENCE 243 AA; 25976 MW; B6FF64D2DCF4F76 CRC64;

Query Match 40.6%; Score 658; DB 2; Length 243;
Best Local Similarity 53.1%; Pred. No. 4.7e-40;
Matches 127; Conservative 43; Mismatches 63; Indels 6; Gaps 4;

QY 3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTIYY 62
Db 1 QVKLQSGSELVRFQASVKLSCKASGYTFTYWHVWVKRQHGQGLEWIGNIYPSGITNY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYYCARDYA---YWGQGTVTYVSSGGG 120
Db 61 DEKFNKGILVTDTSSSTAYMHLSSLASDSAVYCARGGRLDVGAGTTLTVSSGGGG 120

QY 121 SGGGGGGGGSDIELTQSPAIMSAPGERVTMTCSASSV-RYMNWFOQKSGTSPKRWIY 179
Db 121 SGGGGGGGGSDIQMTOSSSFSVSLGDRVTITCKASEDIYRNLAWYQKQKFNAPRLIS 180

QY 180 DTSKLSSGVPARFSGSGTGYSLTISMEADAATYYCQWSSNPLTFAGTKLELK 237
Db 181 GATSLGTVPRFSGSGGKDYTLISLTQIEDVATYYCQYWNSTR--TFGGGKLEIK 237

RESULT 6
```

```
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240188; AAK43733.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER
FT 218
FT 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 37.5%; Score 608.5; DB 2; Length 218;
Best Local Similarity 55.5%; Pred. No. 1.7e-36;
Matches 121; Conservative 33; Mismatches 55; Indels 9; Gaps 3;

QY 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTI 60
Db 1 MAQVKLQSGPELKKPGETVKIRISCKASGYTTTAGMQWVQKMPGKGLKWIWINTHSGVP 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYYCAR-DYG---AYWGQGTVTYVSS 116
Db 61 KYAEFKRFAFSLTSASTAYLQINLKNEDTATYFCMRWDYDGGPAYWGQGTVTYVSS 120

QY 117 GGGGGGGGGGGSDIELTQSPAIMSAPGERVTMTCSASSV-----RYMNWFOQKSG 171
Db 121 GGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESDNIGISFMWVFOQKPG 180

QY 172 TSPKRWIYDTSKLSSGVPARFSGSGTGYSLTISME 209
Db 181 QPPKLLIYAASKQSGVGPAGLLASGSGTDFSLNIYPME 218

RESULT 7
HV16 MOUSE
ID HV16 MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
```



```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RL phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00739; AAA38684.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;

Query Match 31.2%; Score 506; DB 1; Length 107;
Best Local Similarity 90.6%; Pred. No. 2.2e-29; Indels 0; Gaps 0;
Matches 96; Conservative 6; Mismatches 24;

QY 133 IELTQSPAIMSASPGERTVMTCSASSVRYNMVFOOKSGTSPKRWIYDTSKLSGVPARF 192
Db 2 IVLTQSPAIMSASPGQKVTMTCSASSVSYMHYQOKSGTSPKRWIYDTSKLDGVPARF 61

QY 193 SGSGSGTSYSLTISMEAEADAATYYCQWSSNPLTFGAGTKLELKR 238
Db 62 SGSGSATSYSLTITSMQAEADAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 10
KV6I_MOUSE
ID KV6I_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region NQ6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RL phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;

Query Match 30.9%; Score 502; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 4.3e-29; Indels 0; Gaps 0;
Matches 95; Conservative 7; Mismatches 24;

QY 133 IELTQSPAIMSASPGERTVMTCSASSVRYNMVFOOKSGTSPKRWIYDTSKLSGVPARF 192
Db 2 IVLTQSPAIMSASPGQKVTMTCSASSVSYMHYQOKSGTSPKRWIYDTSKLSGXPARF 61

QY 193 SGSGSGTSYSLTISMEAEADAATYYCQWSSNPLTFGAGTKLELKR 238
Db 62 SGSGSATSYSLTITSMQAEADAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 11
KV6G_MOUSE
ID KV6G_MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RL phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K00737; AAA38682.1; -.
DR HSSP; Q91W12; 1AY1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

```

```
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Complementarity-determining-4.
FT DISULFID 23 87 By similarity.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 30.8%; Score 500; DB 1; Length 107;
Best Local Similarity 89.8%; Pred. No. 6.1e-29;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 133 ILTQSPALMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSGVPARF 192
Db 2 ILLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSGVPARF 61
QY 193 SGSGSTSYSLTISMEADAATYTCQWSSNPLTFGAGTKLELKR 238
Db 62 SGSGSATSYSLTISMEADAATYTCQWSSNPLTFGAGTKLELKR 107

RESULT 12
Q8K1F0
ID Q8K1F0 PRELIMINARY; PRT; 112 AA.
AC Q8K1F0
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516285; AAM64203.1; -.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1ORQ.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON TER 1 112
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11901 MW; F664463201AA239 CRC64;

Query Match 30.7%; Score 498; DB 2; Length 112;
Best Local Similarity 88.8%; Pred. No. 8.9e-29;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 135 LTQSPALMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSGVPARFSG 194
Db 4 LTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSGVPARFSG 63
QY 195 SGSGTSYSLTISMEADAATYTCQWSSNPLTFGAGTKLELKR 241
Db 64 SGSGNSYSLTISSTEGDAATYTCQWSSNPLTFGAGTKLELKR 110

RESULT 13
KV6J_MOUSE
ID KV6J_MOUSE STANDARD; PRT; 107 AA.
AC PO4944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC 1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K00744; AAA38689.1; -.
CC HSSP; Q91W12; 1AY1.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00406; IG; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Complementarity-determining-4.
FT DISULFID 23 87 By similarity.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;

Query Match 30.5%; Score 494; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.7e-28;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 133 ILTQSPALMSASPGERVMTTCSSASSVRYMNFQKSGTSPKRWIYDTSKLSGVPARF 192
Db 2 ILLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLSGVPARF 61
QY 193 SGSGSTSYSLTISMEADAATYTCQWSSNPLTFGAGTKLELKR 238
Db 62 XGSGSATSYSLTISMEADAATYTCQWSSNPLTFGAGTKLELKR 107

RESULT 14
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

Search completed: December 30, 2004, 15:54:50  
Job time : 190 secs

**This Page Blank (uspio)**